



- 1 -

SEQUENCE LISTING

<110> Vertino, Paula M.

<120> TMS1 Compositions and Methods of Use

<130> E0355/7003/ERG/MAT

<140> US 09/691,763

<141> 2000-10-18

<150> US 60/159,975

<151> 1999-10-18

<160> 27

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2821

<212> DNA

<213> Homo Sapiens

<400> 1

aagcttttga atacaacatg ctgcaggcat cacagcctca ttcattcctt cactcagcaa	60
atcttactc agcaccta at gtgtccaga tacatttttt ttttcagat ggaatctagc	120
tctgtcaccc aggctggagt gcagtggtgc aatcttgct cactgttagcc tctgcctccg	180
agggtcaagc gattctcatg cctcagccgc ccttagtagct aggattacag gcgcctccca	240
ccacacacag ctatccatcg gtacattctt gacgcttagga attcagcaaa gaataagaca	300
gttaaggctc ccgatgctca taggcctcac attttagaga gggatgaatg tccaataagc	360
atataaacat ataataatgtc agggtcgat gactacaagg aacagtgatt gttacaaccc	420
agatgagagg gaaaaataaa ggattccaaa tatccccctt gggaaatgaga gtcaggattc	480
aaacaaagaa ctgtatgct tcaagttcat ggtcttaat ctcctggagg ctgtctct	540
ttctttttc tttttttaa tcagtgttgg gatcaaattc tggctcccctt aggaagcatc	600
tggcaagggtt tcgggagcca tcgggttggc catgttatgc tggaatattt ataagcaccg	660
gagggttatac cccatgtcg agaaaaatgaa actgaagctc agagagattt gcactctcg	720
cccttttgc taactcattt ttccccatgt tctggaaattt agggagcttc acgcttc	780
ctgtcatgtat tccaagattc tacgacatgt gggagaggat cctaaggttc ggggaaccgc	840
ggagggttgc gggttctaga aatcccgatg tctaagctt ggtctccaa taaaccagg	900
gagagccagc ccaggttcc ggtctgtacc cgctggtgc agccagaga caagcaggcg	960
ccacccatga gcccccttcg gccccctcc cgggtccac ctcgcaggcc agctggaggg	1020
cgcgatcccg cggtccccc acggcctggg gccccaaatcc agaggcctgg gtgggaggg	1080
accaagggtg tagtaaggaa ggccttttg ctggaggggca acggaccggg gccccggatc	1140
gggagaccag agtgggagga aggcggggag tccaggttcc gccccggagc cgacttc	1200
ctggcggcg gctgcagcg ggtgagcgcc ggcagcgcc gggatcccg gagccatggg	1260
gccccggcgc gacgcccccc tggatgcgtt ggagaacctg accggccagg agctcaagaa	1320
gttcaagctg aagctgtgtt cgggtccgtt gcgcgaggcc tacggcgca tccccgggg	1380
cgcgctgtcg tccatggacg ccttggaccc caccgacaaatgttgcgttccatgttcc	1440
gacctacggc gccgagctca ccgcataacgt gctgcgcac atggccctgc aggagatggc	1500
cgggcagctg caggcggcca cgcaccagg tgagccccc ccgttccctt ccaccccgcc	1560
tttccccctcc acccacacca ggccttaccc cgcgggtctt tccgcttccatgttccatgttcc	1620
ccccaaaca aagctgtctt accggaaagg aggtccca cgcttgcctt accgaccaac	1680
gggaccccg gccccacggc ggaaggaaag ggaaggggat cacttggccc atatcctcc	1740
aggctctgga gccgcgcacg ctggatcca ggccttccctt cagtcggcag ccaagccagg	1800
tgaggcctcc acacccagcc cggcccccacc gcactcctgc acagcctgc tctgtgtcc	1860
cgcacccagg gcagggcagg gcagggcagg cacggctgg caaccctgcg caccaccc	1920
accaacccac accctgcggg ggaaggaaag caatattacc ctcatccac tgcattgtgg	1980
gtcctggtgg ccccccctg gagccctgc cctaggctt cagaggaatt cctgaagaac	2040
tcaagttcag caggacacagg ccccacaccc tggctgtgg ctcatgttccatgttccatgttcc	2100

ccagggcctgc actttataga ccagcacccg 2160	gctgcgccta tcgcgagggt cacaacgtt	
gagtggctgc tggatgcctc gtacgggaag gtcctgacgg atgagcagta ccaggcagtg cgcccggagc ccaccaaccc aagcaagatg cgaaagctct tcagttcac accagcctgg aactggacct gcaaggactt gctccctccag gcccctaaggg agtcccagtc ctacctggtg gaggacctgg agcggagctg aggctccctc ccagcaacac tccggtcagc ccctggcaat cccaccaaata catcctgaat ctgatcttt tatacacaaat atacaaaaag ccagcttgaa cttgtgtttt ttcctgcctc tagcctgctg gcatgtgcag agctcagcta tgcttcagag gccaccaggc ctccagctcc atgtccctag ggtctctggc accccaaatg cttccccat ccttcctggt atcgccatgg aatatccctc ctcattcacc aggtgggtct cctccagtg tccctaaagg gtctaacctt accattatac ataacacgct gtgacccagg tccgaaggaa aaaagaggca tgtaccaaag ggcccaaact ggtgggcagc tctgtccaaag ccatttagaa acacactagt cttcatagct cccctacctt ccacatttc cactggaaga aaaaatggca a	2220 2280 2340 2400 2460 2520 2580 2640 2700 2760 2820 2821	
<210> 2		
<211> 770		
<212> DNA		
<213> Homo Sapiens		
<220>		
<221> CDS		
<222> (75) ... (662)		
<400> 2		
ccacgcgtcc gacttcctcc tggtcggcgg ctgcagcggg gtgagcggcg gcagcggccg gggatcctgg agcc atg ggg cgc gcg cgc gac gcc atc ctg gat gcg ctg Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu 1 5 10	60 110	
gag aac ctg acc gcc gag gag ctc aag aag ttc aag ctg aag ctg ctg Glu Asn Leu Thr Ala Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu 15 20 25	158	
tcg gtg ccg ctg cgc gag ggc tac ggg cgc atc ccg cgg ggc gcg ctg Ser Val Pro Leu Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu 30 35 40	206	
ctg tcc atg gac gcc ttg gac ctc acc gac aag ctg gtc agc ttc tac Leu Ser Met Asp Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr 45 50 55 60	254	
ctg gag acc tac ggc gcc gag ctc acc gct aac gtg ctg cgc gac atg Leu Glu Thr Tyr Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met 65 70 75	302	
ggc ctg cag gag atg gcc ggg cag ctg cag gcg gcc acg cac cag ggc Gly Leu Gln Glu Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly 80 85 90	350	
tct gga gcc gcg cca gct ggg atc cag gcc cct cct cag tcg gca gcc Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala 95 100 105	398	
aag cca ggc ctg cac ttt ata gac cag cac cgg gct gcg ctt atc gcg Lys Pro Gly Leu His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala 110 115 120	446	
agg gtc aca aac gtt gag tgg ctg ctg gat gct ctg tac ggg aag gtc Arg Val Thr Asn Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val 125 130 135 140	494	

gggtgagcgg cggcagcggc cggggatcct ggagccatgg ggcgcgcgcg cgacgccatc
180
ctggatgcgc tggagaacct gaccgcgcag gagctcaaga agttcaagct gaagctgctg 240
tcggtgcgc tcgcgcaggc ctacggcgc atcccgcgg gcgcgcgtgc gtccatgac 300
gccttggacc tcaccgacaa gctggtcagc ttctacctgg agacctaagg cgccgagctc 360
accgctaacg tgctgcgcga catgggcctg caggagatgg cgggcagct gcaggcgcc 420
acgcaccagg gtgagccgc cccgtcccc tccacccgt ctttcccctc caccacacc 480
agcgcttacc ccgcggcgc ttccgcttc tgttcctct acccctaaac aaagctgctc 540
taccggaaag gaggctcccc acgcttgcc taccgaccaa cgggaccccg gccccacggc 600
gggaagggaa gggaggga tcactt 626

<210> 5
<211> 340
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> (67)....(339)

<400> 5
ccgacttcct cctggtcggc ggctgcagcg gggtgagcgg cggcagcggc cggggatcct 60
ggagcc atg ggg cgc gcg gac gcc atc ctg gat gcg ctg gag aac 108
Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn
1 5 10

ctg acc gcc gag gag ctc aag aag ttc aag ctg aag ctg ctg tcg gtg 156
Leu Thr Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Ser Val
15 20 25 30

ccg ctg cgc gag ggc tac ggg cgc atc ccg cgg ggc gcg ctg ctg tcc 204
Pro Leu Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser
35 40 45

atg gac gcc ttg gac ctc acc gac aag ctg gtc agc ttc tac ctg gag 252
Met Asp Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu
50 55 60

acc tac ggc gcc gag ctc acc gct aac gtg ctg cgc gac atg ggc ctg 300
Thr Tyr Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu
65 70 75

cag gag atg gcc ggg cag ctg cag gcg gcc acg cac cag g 340
Gln Glu Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln
80 85 90

<210> 6
<211> 91
<212> PRT
<213> Homo Sapiens

<400> 6
Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr
1 5 10 15
Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val Pro Leu
20 25 30
Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser Met Asp
35 40 45
Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr
50 55 60

Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu
65 70 75 80
Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln
85 90

<210> 7
<211> 57
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> (3)...(56)

<400> 7
gc tct gga gcc gca gct ggg atc cag gcc cct cct cag tcg gca 47
Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala
1 5 10 15
gcc aag cca g 57
Ala Lys Pro

<210> 8
<211> 18
<212> PRT
<213> Homo Sapiens

<400> 8
Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala
1 5 10 15
Lys Pro

<210> 9
<211> 356
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> (3)...(258)

<400> 9
gc ctg cac ttt ata gac cag cac cgg gct gcg ctt atc gcg agg gtc 47
Leu His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val
1 5 10 15

aca aac gtt gag tgg ctg ctg gat gct ctg tac ggg aag gtc ctg acg 95
Thr Asn Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr
20 25 30

gat gag cag tac cag gca gtg cgg gcc gag ccc acc aac cca agc aag 143
Asp Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys
35 40 45

atg cgg aag ctc ttc agt ttc aca cca gcc tgg aac tgg acc tgc aag 191
Met Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys
50 55 60

gac ttg ctc ctc cag gcc cta agg gag	65	tcc cag tcc tac ctg gtg gag	70	75	239
Asp Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu					
ctggcaatcc caccaaatac tcctgaatct gatctttta tacacaatat acgaaaagcc					348
agcttgaa					356
<210> 10					
<211> 84					
<212> PRT					
<213> Homo Sapiens					
<400> 10					
Leu His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr	1	5	10	15	
Asn Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp	20	25	30		
Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met	35	40	45		
Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp	50	55	60		
Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp	65	70	75	80	
Leu Glu Arg Ser					
<210> 11					
<211> 18					
<212> DNA					
<213> Homo Sapiens					
<400> 11					
gcactttata gaccagca					18
<210> 12					
<211> 18					
<212> DNA					
<213> Homo Sapiens					
<400> 12					
attttgtggg attgccag					18
<210> 13					
<211> 17					
<212> DNA					
<213> Homo Sapiens					
<400> 13					
tgggcctgca ggagatg					17
<210> 14					
<211> 22					
<212> DNA					
<213> Homo Sapiens					
<400> 14					
ccttcctggg catggagtcc tg					22

<210> 15
<211> 21
<212> DNA
<213> Homo Sapiens

<400> 15
ggagcaatga tcttgatctt c 21

<210> 16
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Primer

<400> 16
ggttgttagtg gggtagtgg t 21

<210> 17
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Primer

<400> 17
. caaaacatcc ataaaacaaca acaca 25

<210> 18
<211> 19
<212> DNA
<213> Homo Sapiens

<400> 18
ttgttagcggt gtgagcggc 19

<210> 19
<211> 22
<212> DNA
<213> Homo Sapiens

<400> 19
aacgtccata aacaacaacg cg 22

<210> 20
<211> 803
<212> DNA
<213> Mus Musculus

<220>
<221> CDS
<222> (162)...(743)

<400> 20
gggaaagaac aggagctgta agaaaagagg gtgggggagt cccagcatgc ccatcgccct 60
aagcagctga ctccctggtc ttggcggtc ggcagcaggc aggctgagca ggcgagcagc 120
agcaagagta aaaggtgacc gcggctgcc accccagagc c atg ggg cgg gca cga 176
Met Gly Arg Ala Arg

gat gcc atc ctg gac gct ctt gaa aac ttg tca ggg gat gaa ctc aaa Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Ser Gly Asp Glu Leu Lys 10 15 20	224
aag ttc aag atg aag ctg ctg aca gtg caa ctg cga gaa ggc tat ggg Lys Phe Lys Met Lys Leu Leu Thr Val Gln Leu Arg Glu Gly Tyr Gly 25 30 35	272
cgc atc cca cgc ggg gcc ctg ctg cag atg gac gcc ata gat ctc act Arg Ile Pro Arg Gly Ala Leu Leu Gln Met Asp Ala Ile Asp Leu Thr 40 45 50	320
gac aaa ctt gtc agc tac tat ctg gag tcg tat ggc ttg gag ctc aca Asp Lys Leu Val Ser Tyr Tyr Leu Glu Ser Tyr Gly Leu Glu Leu Thr 55 60 65	368
atg act gtg ctt aga gac atg ggc tta cag gag ctg gct gag cag ctg Met Thr Val Leu Arg Asp Met Gly Leu Gln Glu Leu Ala Glu Gln Leu 70 75 80 85	416
caa acg act aaa gaa gag tct gga gct gtg gca gct gca gcc agt gtc Gln Thr Thr Lys Glu Glu Ser Gly Ala Val Ala Ala Ala Ser Val 90 95 100	464
cct gct cag agt aca gcc aga aca gga cac ttt gtg gac cag cac agg Pro Ala Gln Ser Thr Ala Arg Thr Gly His Phe Val Asp Gln His Arg 105 110 115	512
caa gca ctc att gcc agg gtc aca gaa gtg gac gga gtg ctg gat gct Gln Ala Leu Ile Ala Arg Val Thr Glu Val Asp Gly Val Leu Asp Ala 120 125 130	560
ttg cat ggc agt gtg ctg act gaa gga cag tac cag gca gtt cgt gca Leu His Gly Ser Val Leu Thr Glu Gly Gln Tyr Gln Ala Val Arg Ala 135 140 145	608
gag acc acc agc caa gac aag atg agg aag ctc ttc agc ttt gtt cca Glu Thr Thr Ser Gln Asp Lys Met Arg Lys Leu Phe Ser Phe Val Pro 150 155 160 165	656
tcc tgg aac ctg acc tgc aag gac tcc ctc ctc cag gcc ttg aag gaa Ser Trp Asn Leu Thr Cys Lys Asp Ser Leu Leu Gln Ala Leu Lys Glu 170 175 180	704
ata cat ccc tac ttg gtg atg gac ctg gag cag agc tga ggtatctttt Ile His Pro Tyr Leu Val Met Asp Leu Glu Gln Ser *185 190	753
ccagctacat tatcttagctc ctgactttgt atacacaatt tttgaaaaaaaa	803
<210> 21	
<211> 193	
<212> PRT	
<213> Mus Musculus	
<400> 21	
Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Ser 1 5 10 15	
Gly Asp Glu Leu Lys Lys Phe Lys Met Lys Leu Leu Thr Val Gln Leu	

20	25	30
Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Gln Met Asp		
35	40	45
Ala Ile Asp Leu Thr Asp Lys Leu Val Ser Tyr Tyr Leu Glu Ser Tyr		
50	55	60
Gly Leu Glu Leu Thr Met Thr Val Leu Arg Asp Met Gly Leu Gln Glu		
65	70	75
Leu Ala Glu Gln Leu Gln Thr Thr Lys Glu Glu Ser Gly Ala Val Ala		80
85	90	95
Ala Ala Ala Ser Val Pro Ala Gln Ser Thr Ala Arg Thr Gly His Phe		
100	105	110
Val Asp Gln His Arg Gln Ala Leu Ile Ala Arg Val Thr Glu Val Asp		
115	120	125
Gly Val Leu Asp Ala Leu His Gly Ser Val Leu Thr Glu Gly Gln Tyr		
130	135	140
Gln Ala Val Arg Ala Glu Thr Thr Ser Gln Asp Lys Met Arg Lys Leu		
145	150	155
Phe Ser Phe Val Pro Ser Trp Asn Leu Thr Cys Lys Asp Ser Leu Leu		160
165	170	175
Gln Ala Leu Lys Glu Ile His Pro Tyr Leu Val Met Asp Leu Glu Gln		
180	185	190
Ser		

<210> 22
<211> 605
<212> DNA
<213> Rattus Norvegicus

<220>
<221> CDS
<222> (2)...(518)

<400> 22

t ttc aag ata aag ctg ctg aca gcg cca gtg cg ^g gaa ggc tat ggg cgc	49	
Phe Lys Ile Lys Leu Leu Thr Ala Pro Val Arg Glu Gly Tyr Gly Arg		
1	5	10
		15
atc cca cgg ggg gcc ctg ctg cag atg gac ccc ata gac ctc act gat	97	
Ile Pro Arg Gly Ala Leu Leu Gln Met Asp Pro Ile Asp Leu Thr Asp		
20	25	30
aaa ctc gtc agy tac tat ctg gag ggg tat ggc ttg gag ctc aca atg	145	
Lys Leu Val Xaa Tyr Tyr Leu Glu Gly Tyr Gly Leu Glu Leu Thr Met		
35	40	45
act gtg ctt aga gac atg ggc ata cag gag ctg gct gag cag ctg caa	193	
Thr Val Leu Arg Asp Met Gly Ile Gln Glu Leu Ala Glu Gln Leu Gln		
50	55	60
aag att atg gaa gag tct gga gct gtg gct act gca acc agt gtc cct	241	
Lys Ile Met Glu Glu Ser Gly Ala Val Ala Thr Ala Thr Ser Val Pro		
65	70	75
		80
gct cag ggc aca gcc aga aca gaa cat ttt gtg gac caa cac agg caa	289	
Ala Gln Gly Thr Ala Arg Thr Glu His Phe Val Asp Gln His Arg Gln		
85	90	95
gca ctc att gcc agg gtc aca gaa gtt gat ggt ttg ctg gat gct ctg	337	
Ala Leu Ile Ala Arg Val Thr Glu Val Asp Gly Leu Leu Asp Ala Leu		
100	105	110

tat ggc aat gtg ctg act gaa gga cag tac cag gca gtt cgt gca gag 385
Tyr Gly Asn Val Leu Thr Glu Gly Gln Tyr Gln Ala Val Arg Ala Glu
115 120 125

acc acc aac caa aac aag atg agg aag ctc ttt agc ttt gct cca gcc 433
Thr Thr Asn Gln Asn Lys Met Arg Lys Leu Phe Ser Phe Ala Pro Ala
130 135 140

tgg aac ctg acc tgc aag aac ttg ttc ctt gag gcc ttg agg caa aca 481
Trp Asn Leu Thr Cys Lys Asn Leu Phe Leu Glu Ala Leu Arg Gln Thr
145 150 155 160

cag ccc tac ttg gtg aca gac ctg gaa cag agc tga g gtatctttc 528
Gln Pro Tyr Leu Val Thr Asp Leu Glu Gln Ser *
165 170

cagctacaca tctagctcct ggttttgtat acaaaaattt ctaaaaacaa gtttgtattt 588
gtgtttctc gaaaaaa 605

<210> 23
<211> 171
<212> PRT
<213> Rattus Norvegicus

<220>
<223> Xaa can be any amino acid.

<400> 23
Phe Lys Ile Lys Leu Leu Thr Ala Pro Val Arg Glu Gly Tyr Gly Arg
1 5 10 15
Ile Pro Arg Gly Ala Leu Leu Gln Met Asp Pro Ile Asp Leu Thr Asp
20 25 30
Lys Leu Val Xaa Tyr Tyr Leu Glu Gly Tyr Gly Leu Glu Leu Thr Met
35 40 45
Thr Val Leu Arg Asp Met Gly Ile Gln Glu Leu Ala Glu Gln Leu Gln
50 55 60
Lys Ile Met Glu Glu Ser Gly Ala Val Ala Thr Ala Thr Ser Val Pro
65 70 75 80
Ala Gln Gly Thr Ala Arg Thr Glu His Phe Val Asp Gln His Arg Gln
85 90 95
Ala Leu Ile Ala Arg Val Thr Glu Val Asp Gly Leu Leu Asp Ala Leu
100 105 110
Tyr Gly Asn Val Leu Thr Glu Gly Gln Tyr Gln Ala Val Arg Ala Glu
115 120 125
Thr Thr Asn Gln Asn Lys Met Arg Lys Leu Phe Ser Phe Ala Pro Ala
130 135 140
Trp Asn Leu Thr Cys Lys Asn Leu Phe Leu Glu Ala Leu Arg Gln Thr
145 150 155 160
Gln Pro Tyr Leu Val Thr Asp Leu Glu Gln Ser
165 170

<210> 24
<211> 713
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> (75)...(605)

<400> 24
ccacgcgtcc gacttcctcc tggcggcg ctgcagcgaa gtgagcgccg gcagcgcccc 60
gggatccctgg agcc atg ggg cgc gcg cgc gac gcc atc ctg gat gcg ctg 110
Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu
1 5 10

gag aac ctg acc gcc gag gag ctc aag aag ttc aag ctg aag ctg ctg 158
Glu Asn Leu Thr Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu
15 20 25

tcg gtg ccg ctg cgc gag ggc tac ggg cgc atc ccg cgg ggc gcg ctg 206
Ser Val Pro Leu Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu
30 35 40

ctg tcc atg gac gcc ttg gac ctc acc gac aag ctg gtc agc ttc tac 254
Leu Ser Met Asp Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr
45 50 55 60

ctg gag acc tac ggc gcc gag ctc acc gct aac gtg ctg cgc gac atg 302
Leu Glu Thr Tyr Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met
65 70 75

ggc ctg cag gag atg gcc ggg cag ctg cag gcg gcc acg cac cag ggc 350
Gly Leu Gln Glu Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly
80 85 90

ctg cac ttt ata gac cag cac cgg gct gcg ctt atc gcg agg gtc aca 398
Leu His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr
95 100 105

aac gtt gag tgg ctg ctg gat gct ctg tac ggg aag gtc ctg acg gat 446
Asn Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp
110 115 120

gag cag tac cag gca gtg cgg gcc gag ccc acc aac cca agc aag atg 494
Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met
125 130 135 140

cgg aag ctc ttc agt ttc aca cca gcc tgg aac tgg acc tgc aag gac 542
Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp
145 150 155

ttg ctc ctc cag gcc cta agg gag tcc cag tcc tac ctg gtg gag gac 590
Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp
160 165 170

ctg gag cgg agc tga ggctccttcc cagcaacact ccggtcagcc cctggcaatc 645
Leu Glu Arg Ser *
175

ccaccaaatac atcctgaatc tgatctttt atacacaata tacgaaaagc cagcttgaaa 705
aaaaaaaaa 713

<210> 25
<211> 176
<212> PRT
<213> Homo Sapiens

<400> 25
Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr
1 5 10 15

Ala Glu Glu Leu Lys Lys Phe Lys	20	25	Leu Lys Leu Leu Ser Val Pro Leu	30
Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser Met Asp	35	40	45	
Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr	50	55	60	
Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu	65	70	75	80
Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly Leu His Phe Ile	85	90	95	
Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr Asn Val Glu Trp	100	105	110	
Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp Glu Gln Tyr Gln	115	120	125	
Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met Arg Lys Leu Phe	130	135	140	
Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp Leu Leu Leu Gln	145	150	155	160
Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp Leu Glu Arg Ser	165	170	175	

<210> 26
<211> 405
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> (75)...(404)

<400> 26

ccacgcgtcc gacttcctcc tggtcggcgg ctgcagcggg gtgagcggcg gcagcggccg	60
gggatcctgg agcc atg ggg cgc gcg cgc gac gcc atc ctg gat gcg ctg	110
Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu	
1 5 10	
gag aac ctg acc gcc gag gag ctc aag aag ttc aag ctg aag ctg ctg	158
Glu Asn Leu Thr Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu	
15 20 25	
tcg gtg ccg ctg cgc gag ggc tac ggg cgc atc ccg ccg ggc gcg ctg	206
Ser Val Pro Leu Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu	
30 35 40	
ctg tcc atg gac gcc ttg gac ctc acc gac aag ctg gtc agc ttc tac	254
Leu Ser Met Asp Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr	
45 50 55 60	
ctg gag acc tac ggc gcc gag ctc acc gct aac gtg ctg cgc gac atg	302
Leu Glu Thr Tyr Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met	
65 70 75	
ggc ctg cag gag atg gcc ggg cag ctg cag gcg gcc acg cac cag ggc	350
Gly Leu Gln Glu Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly	
80 85 90	
tct gga gcc gcg cca gct ggg atc cag gcc cct cct cag tcg gca gcc	398
Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala	
95 100 105	
aag cca g	405

Lys Pro
110

<210> 27
<211> 110
<212> PRT
<213> Homo Sapiens

<400> 27
Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr
1 5 10 15
Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val Pro Leu
20 25 30
Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser Met Asp
35 40 45
Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr
50 55 60
Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu
65 70 75 80
Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly Ser Gly Ala Ala
85 90 95
Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala Lys Pro
100 105 110